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1642

RAW SEQUENCE LISTING

DATE: 02/06/2002

PATENT APPLICATION: US/09/654,281B

TIME: 08:50:53

Input Set : A:\ES.txt

Output Set: N:\CRF3\02062002\I654281B.raw

p.5

3 <110> APPLICANT: Sedivy, John
 4 Kolch, Walter
 5 Yeung, Kam Chi
 7 <120> TITLE OF INVENTION: Kinase Inhibitors and Methods of Use in Screening Assays and
 Modulation
 8 of Cell Proliferation and Growth
 10 <130> FILE REFERENCE: 3564/1010
 12 <140> CURRENT APPLICATION NUMBER: 09/654,281B
 13 <141> CURRENT FILING DATE: 2000-09-01
 15 <150> PRIOR APPLICATION NUMBER: 60/151,992
 16 <151> PRIOR FILING DATE: 1999-09-01
 18 <160> NUMBER OF SEQ ID NOS: 11
 20 <170> SOFTWARE: PatentIn version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 94
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Artificial Sequence
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: consensus sequence
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 31 <221> NAME/KEY: MISC_FEATURE
 32 <222> LOCATION: (3)..(5)
 33 <223> OTHER INFORMATION: Xaa = any amino acid
 36 <220> FEATURE:
 37 <221> NAME/KEY: MISC_FEATURE
 38 <222> LOCATION: (9)..(9)
 39 <223> OTHER INFORMATION: a hydrophobic amino acid residue
 42 <220> FEATURE:
 43 <221> NAME/KEY: MISC_FEATURE
 44 <222> LOCATION: (11)..(13)
 45 <223> OTHER INFORMATION: Xaa = any amino acid
 48 <220> FEATURE:
 49 <221> NAME/KEY: MISC_FEATURE
 50 <222> LOCATION: (14)..(14)
 51 <223> OTHER INFORMATION: a negatively charged amino acid residue
 54 <220> FEATURE:
 55 <221> NAME/KEY: MISC_FEATURE
 56 <222> LOCATION: (15)..(18)
 57 <223> OTHER INFORMATION: Xaa = any amino acid residue
 60 <220> FEATURE:
 61 <221> NAME/KEY: MISC_FEATURE
 62 <222> LOCATION: (20)..(21)
 63 <223> OTHER INFORMATION: Xaa = any amino acid residue
 66 <220> FEATURE:

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67 <221> NAME/KEY: MISC_FEATURE
68 <222> LOCATION: (23)..(72)
69 <223> OTHER INFORMATION: Xaa = any amino acid residue, 0 to 40 residues may be missing
72 <220> FEATURE:
73 <221> NAME/KEY: MISC_FEATURE
74 <222> LOCATION: (74)..(77)
75 <223> OTHER INFORMATION: Xaa = any amino acid residue
78 <220> FEATURE:
79 <221> NAME/KEY: MISC_FEATURE
80 <222> LOCATION: (79)..(82)
81 <223> OTHER INFORMATION: Xaa = any amino acid residue, 0 to 2 residues may be missing
84 <220> FEATURE:
85 <221> NAME/KEY: MISC_FEATURE
86 <222> LOCATION: (84)..(84)
87 <223> OTHER INFORMATION: Xaa = any amino acid residue
90 <220> FEATURE:
91 <221> NAME/KEY: MISC_FEATURE
92 <222> LOCATION: (87)..(87)
93 <223> OTHER INFORMATION: Xaa = an aromatic amino acid residue
96 <220> FEATURE:
97 <221> NAME/KEY: MISC_FEATURE
98 <222> LOCATION: (89)..(89)
99 <223> OTHER INFORMATION: Xaa = any amino acid residue
102 <220> FEATURE:
103 <221> NAME/KEY: MISC_FEATURE
104 <222> LOCATION: (90)..(90)
105 <223> OTHER INFORMATION: a hydrophobic amino acid residue
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109 <221> NAME/KEY: MISC_FEATURE
110 <222> LOCATION: (91)..(93)
111 <223> OTHER INFORMATION: Xaa = any amino acid residue
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      117 1 5 10 15
W--> 120 Xaa Xaa Glu Xaa Xaa His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      121 20 25 30
W--> 124 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      125 35 40 45
W--> 128 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      129 50 55 60
W--> 132 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Pro Xaa Xaa
      133 65 70 75 80
W--> 136 Xaa Xaa Gly Xaa His Arg Xaa Val Xaa Glx Xaa Xaa Xaa Gln
      137 85 90
140 <210> SEQ ID NO: 2
141 <211> LENGTH: 187
142 <212> TYPE: PRT
143 <213> ORGANISM: Homo sapiens
145 <400> SEQUENCE: 2

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147 Met Pro Val Asp Leu Ser Lys Trp Ser Gly Pro Leu Ser Leu Gln Glu
148 1          5          10          15
151 Val Asp Glu Gln Pro Gln His Pro Leu His Val Thr Tyr Ala Gly Ala
152          20          25          30
155 Ala Val Asp Glu Leu Gly Lys Val Leu Thr Pro Thr Gln Val Lys Asn
156          35          40          45
159 Arg Pro Thr Ser Ile Ser Trp Asp Gly Leu Asp Ser Gly Lys Leu Tyr
160          50          55          60
163 Thr Leu Val Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Asp Pro Lys
164 65          70          75          80
167 Tyr Arg Glu Trp His His Phe Leu Val Val Asn Met Lys Gly Asn Asp
168          85          90          95
171 Ile Ser Ser Gly Thr Val Leu Ser Asp Tyr Val Gly Ser Gly Pro Pro
172          100          105          110
175 Lys Gly Thr Gly Leu His Arg Tyr Val Trp Leu Val Tyr Glu Gln Asp
176          115          120          125
179 Arg Pro Leu Lys Cys Asp Glu Pro Ile Leu Ser Asn Arg Ser Gly Lys
180          130          135          140
183 His Arg Gly Lys Phe Lys Val Ala Ser Phe Arg Lys Lys Tyr Glu Leu
184 145          150          155          160
187 Arg Ala Pro Val Ala Gly Thr Cys Tyr Gln Ala Glu Trp Lys Lys Tyr
188          165          170          175
191 Val Pro Lys Leu Tyr Glu Gln Leu Ser Gly Lys
192          180          185
195 <210> SEQ ID NO: 3
196 <211> LENGTH: 187
197 <212> TYPE: PRT
198 <213> ORGANISM: Mus musculus
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201 <221> NAME/KEY: MISC_FEATURE
202 <222> LOCATION: (150)..(150)
203 <223> OTHER INFORMATION: Xaa = any amino acid residue
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209 1          5          10          15
212 Val Asp Glu Pro Pro Gln His Ala Leu Arg Val Asp Tyr Ala Gly Val
213          20          25          30
216 Thr Val Asp Glu Leu Gly Lys Val Leu Thr Pro Thr Gln Val Met Asn
217          35          40          45
220 Arg Pro Ser Ser Ile Ser Trp Asp Gly Leu Asp Pro Gly Lys Leu Tyr
221          50          55          60
224 Thr Leu Val Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Asp Pro Lys
225 65          70          75          80
228 Phe Arg Glu Trp His His Phe Leu Val Val Asn Met Lys Gly Asn Asp
229          85          90          95
232 Ile Ser Ser Gly Thr Val Leu Ser Asp Tyr Val Gly Ser Gly Pro Pro
233          100          105          110
236 Ser Gly Thr Ser Ile His Arg Tyr Val Trp Leu Val Tyr Glu Gln Glu
237          115          120          125

```

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Input Set : A:\ES.txt

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240 Gln Pro Leu Ser Cys Asp Glu Pro Ile Leu Ser Asn Lys Ser Gly Asp
 241 130 135 140
 244 Asn Arg Gly Lys Phe Xaa Val Glu Thr Phe Arg Lys Lys Tyr Asn Leu
 245 145 150 155 160
 248 Gly Ala Pro Val Ala Gly Thr Cys Tyr Gln Ala Glu Trp Asp Asp Tyr
 249 165 170 175
 252 Val Pro Lys Leu Tyr Glu Gln Leu Ser Gly Lys
 253 180 185
 256 <210> SEQ ID NO: 4
 257 <211> LENGTH: 187
 258 <212> TYPE: PRT
 259 <213> ORGANISM: Drosophila
 261 <400> SEQUENCE: 4
 263 Met Ser Asp Ser Thr Val Cys Phe Ser Lys His Lys Ile Val Pro Asp
 264 1 5 10 15
 267 Ile Leu Lys Thr Cys Pro Ala Thr Leu Leu Thr Val Thr Tyr Gly Gly
 268 20 25 30
 271 Gly Gln Val Val Asp Val Gly Gly Glu Leu Thr Pro Thr Gln Val Gln
 272 35 40 45
 275 Ser Gln Pro Lys Val Lys Trp Asp Ala Asp Pro Asn Ala Phe Tyr Thr
 276 50 55 60
 279 Leu Leu Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Glu Pro Lys Phe
 280 65 70 75 80
 283 Arg Glu Trp His His Trp Leu Val Val Asn Ile Pro Gly Asn Gln Val
 284 85 90 95
 287 Glu Asn Gly Val Val Leu Thr Glu Tyr Val Gly Ala Gly Pro Pro Gln
 288 100 105 110
 291 Gly Thr Gly Leu His Arg Tyr Val Phe Ile Val Phe Lys Gln Pro Gln
 292 115 120 125
 295 Lys Leu Thr Cys Asn Glu Pro Lys Ile Pro Lys Thr Ser Gly Asp Lys
 296 130 135 140
 299 Arg Ala Asn Phe Ser Thr Ser Lys Phe Met Ser Lys Tyr Lys Leu Gly
 300 145 150 155 160
 303 Asp Pro Ile Ala Gly Asn Phe Phe Gln Ala Gln Trp Asp Asp Tyr Val
 304 165 170 175
 307 Pro Lys Leu Tyr Lys Gln Leu Ser Gly Lys Lys
 308 180 185
 311 <210> SEQ ID NO: 5
 312 <211> LENGTH: 220
 313 <212> TYPE: PRT
 314 <213> ORGANISM: C. elegans
 316 <400> SEQUENCE: 5
 318 Met Val Val Leu Val Thr Arg Ser Leu Leu Pro Ala Leu Phe Phe Ala
 319 1 5 10 15
 322 Ser Arg Ala Pro Phe Ala Ala Ala Thr Thr Ser Ala Arg Phe Gln Arg
 323 20 25 30
 326 Gly Leu Ala Thr Met Ala Ala Glu Ala Phe Thr Lys His Glu Val Ile
 327 35 40 45
 330 Pro Asp Val Leu Ala Ser Asn Pro Pro Ser Lys Val Val Ser Val Lys

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Input Set : A:\ES.txt

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331      50              55              60
334 Phe Asn Ser Gly Val Glu Ala Asn Leu Gly Asn Val Leu Thr Pro Thr
335 65              70              75              80
338 Gln Val Lys Asp Thr Pro Glu Val Lys Trp Asp Ala Glu Pro Gly Ala
339      85              90              95
342 Leu Tyr Thr Leu Thr Lys Thr Asp Pro Asp Ala Pro Ser Arg Lys Glu
343      100             105             110
346 Pro Thr Tyr Arg Glu Trp His His Trp Leu Val Val Asn Ile Pro Gly
347      115             120             125
350 Asn Asp Ile Ala Lys Gly Asp Thr Leu Ser Glu Tyr Ile Gly Ala Gly
351      130             135             140
354 Pro Pro Lys Thr Gly Leu His Arg Tyr Val Tyr Leu Ile Tyr Lys Gln
355 145             150             155             160
358 Ser Gly Arg Ile Glu Asp Ala Glu His Gly Arg Leu Thr Asn Thr Ser
359      165             170             175
362 Gly Asp Lys Arg Gly Gly Trp Lys Ala Ala Asp Phe Val Ala Lys His
363      180             185             190
366 Lys Leu Gly Ala Pro Val Phe Gly Asn Leu Phe Gln Ala Glu Tyr Asp
367      195             200             205
370 Asp Tyr Val Pro Ile Leu Asn Lys Gln Leu Gly Ala
371      210             215             220
374 <210> SEQ ID NO: 6
375 <211> LENGTH: 181
376 <212> TYPE: PRT
377 <213> ORGANISM: Antirrhinum-CEN
379 <400> SEQUENCE: 6
381 Met Ala Ala Lys Val Ser Ser Asp Pro Leu Val Ile Gly Arg Val Ile
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385 Gly Asp Val Val Asp His Phe Thr Ser Thr Val Lys Met Ser Val Ile
386      20              25              30
389 Tyr Asn Ser Asn Asn Ser Ile Lys His Val Tyr Asn Gly His Glu Leu
390      35              40              45
393 Phe Pro Ser Ala Val Thr Ser Thr Pro Arg Val Glu Val His Gly Gly
394      50              55              60
397 Asp Met Arg Ser Phe Phe Thr Leu Ile Met Thr Asp Pro Asp Val Pro
398 65              70              75              80
401 Gly Pro Ser Asp Pro Tyr Leu Arg Glu His Leu His Trp Ile Val Thr
402      85              90              95
405 Asp Ile Pro Gly Thr Thr Asp Ser Ser Phe Gly Lys Glu Val Val Ser
406      100             105             110
409 Tyr Glu Met Pro Arg Pro Asn Ile Gly Ile His Arg Phe Val Phe Leu
410      115             120             125
413 Leu Phe Lys Gln Lys Lys Arg Gly Gln Ala Met Leu Ser Pro Pro Val
414      130             135             140
417 Val Cys Arg Asp Gly Phe Asn Thr Arg Lys Phe Thr Gln Glu Asn Glu
418 145             150             155             160
421 Leu Gly Leu Pro Val Ala Ala Val Phe Phe Asn Cys Gln Arg Glu Thr
422      165             170             175
425 Ala Ala Arg Arg Arg

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\ES.txt

Output Set: N:\CRF3\02062002\I654281B.raw

L:116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:561 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:581 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11